

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/6/5,383A  
Source: 1FW/6  
Date Processed by STIC: 8/21/06

# ***ENTERED***



IFW16

## RAW SEQUENCE LISTING

DATE: 08/21/2006

PATENT APPLICATION: US/10/615,383A

TIME: 11:35:13

Input Set : A:\Sequence\_10-615,383.txt

Output Set : N:\CRF4\08212006\J615383A.raw

5 <110> APPLICANT: FOSTER, Timothy  
 7 <120> TITLE OF INVENTION: POLYPEPTIDES AND POLYNUCLEOTIDES FROM COAGULASE-NEGATIVE  
 STAPHYLOCOCCI

9 <130> FILE REFERENCE: P06335US03/BAS  
 11 <140> CURRENT APPLICATION NUMBER: 10/615,383A  
 12 <141> CURRENT FILING DATE: 2003-07-09  
 14 <150> PRIOR APPLICATION NUMBER: 09/386,962  
 15 <151> PRIOR FILING DATE: 1999-08-31  
 17 <150> PRIOR APPLICATION NUMBER: 60/098,443  
 18 <151> PRIOR FILING DATE: 1998-08-31  
 20 <150> PRIOR APPLICATION NUMBER: 60/117,119  
 21 <151> PRIOR FILING DATE: 1999-01-25  
 23 <160> NUMBER OF SEQ ID NOS: 40  
 25 <170> SOFTWARE: PatentIn version 3.1  
 27 <210> SEQ ID NO: 1  
 28 <211> LENGTH: 5406  
 29 <212> TYPE: DNA  
 30 <213> ORGANISM: Staphylococcus epidermidis  
 32 <220> FEATURE:  
 33 <221> NAME/KEY: CDS  
 34 <222> LOCATION: (1)..(5406)  
 35 <223> OTHER INFORMATION:

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40	1 5 10 15	
42	aat tta caa gta aat att caa att att tcc ttg taa aat att tat ttt	96
43	Asn Leu Gln Val Asn Ile Gln Ile Ile Ser Leu Asn Ile Tyr Phe	
44	20 25 30	
46	aac tgg agg tat agt atg aaa aag aga aga caa gga cca att aac aag	144
47	Asn Trp Arg Tyr Ser Met Lys Lys Arg Arg Gln Gly Pro Ile Asn Lys	
48	35 40 45	
50	aga gtg gat ttt cta tcc aac aag gta aac aag tac tcg att agg aag	192
51	Arg Val Asp Phe Leu Ser Asn Lys Val Asn Lys Tyr Ser Ile Arg Lys	
52	50 55 60	
54	ttc aca gta ggt aca gct tca ata ctc gtg ggt gct acg tta atg ttt	240
55	Phe Thr Val Gly Thr Ala Ser Ile Leu Val Gly Ala Thr Leu Met Phe	
56	65 70 75	
58	ggt gcc gca gac aat gag gct aaa gcg gct gaa gac aat caa tta gaa	288
59	Gly Ala Ala Asp Asn Glu Ala Lys Ala Ala Glu Asp Asn Gln Leu Glu	
60	80 85 90	
62	tca gct tca aaa gaa gaa cag aaa ggt agt cgt gat aat gaa aac tca	336
63	Ser Ala Ser Lys Glu Glu Gln Lys Gly Ser Arg Asp Asn Glu Asn Ser	
64	95 100 105 110	

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67 Lys Leu Asn Gln Val Asp Leu Asp Asn Gly Ser His Ser Ser Glu Lys
68          115          120          125
70 aca aca aat gta aac aat gca act gaa gta aaa aaa gtt gaa gca cca      432
71 Thr Thr Asn Val Asn Asn Ala Thr Glu Val Lys Lys Val Glu Ala Pro
72          130          135          140
74 acg aca agt gac gta tct aag cct aaa gct aat gaa gca gta gtg acg      480
75 Thr Thr Ser Asp Val Ser Lys Pro Lys Ala Asn Glu Ala Val Val Thr
76          145          150          155
78 aat gag tca act aaa cca aaa aca aca gaa gca cca act gtt aat gag      528
79 Asn Glu Ser Thr Lys Pro Lys Thr Thr Glu Ala Pro Thr Val Asn Glu
80          160          165          170
82 gaa tca ata gct gaa aca ccc aaa acc tca act aca caa caa gat tcg      576
83 Glu Ser Ile Ala Glu Thr Pro Lys Thr Ser Thr Thr Gln Gln Asp Ser
84 175          180          185          190
86 act gag aag aat aat cca tct tta aaa gat aat tta aat tca tcc tca      624
87 Thr Glu Lys Asn Asn Pro Ser Leu Lys Asp Asn Leu Asn Ser Ser Ser
88          195          200          205
90 acg aca tct aaa gaa agt aaa aca gac gaa cat tct act aag caa gct      672
91 Thr Thr Ser Lys Glu Ser Lys Thr Asp Glu His Ser Thr Lys Gln Ala
92          210          215          220
94 caa atg tct act aat aaa tca aat tta gac aca aat gac tct cca act      720
95 Gln Met Ser Thr Asn Lys Ser Asn Leu Asp Thr Asn Asp Ser Pro Thr
96          225          230          235
98 caa agt gag aaa act tca tca caa gca aat aac gac agt aca gat aat      768
99 Gln Ser Glu Lys Thr Ser Ser Gln Ala Asn Asn Asp Ser Thr Asp Asn
100          240          245          250
102 cag tca gca cct tct aaa caa tta gat tca aaa cca tca gaa caa aaa      816
103 Gln Ser Ala Pro Ser Lys Gln Leu Asp Ser Lys Pro Ser Glu Gln Lys
104 255          260          265          270
106 gta tat aaa aca aaa ttt aat gat gaa cct act caa gat gtt gaa cac      864
107 Val Tyr Lys Thr Lys Phe Asn Asp Glu Pro Thr Gln Asp Val Glu His
108          275          280          285
110 acg aca act aaa tta aaa aca cct tct gtt tca aca gat agt tca gtc      912
111 Thr Thr Thr Lys Leu Lys Thr Pro Ser Val Ser Thr Asp Ser Ser Val
112          290          295          300
114 aat gat aag caa gat tac aca cga agt gct gta gct agt tta ggt gtt      960
115 Asn Asp Lys Gln Asp Tyr Thr Arg Ser Ala Val Ala Ser Leu Gly Val
116          305          310          315
118 gat tct aat gaa aca gaa gca att aca aat gca gtt aga gac aat tta      1008
119 Asp Ser Asn Glu Thr Glu Ala Ile Thr Asn Ala Val Arg Asp Asn Leu
120          320          325          330
122 gat tta aaa gct gca tct aga gaa caa atc aat gaa gca atc att gct      1056
123 Asp Leu Lys Ala Ala Ser Arg Glu Gln Ile Asn Glu Ala Ile Ile Ala
124 335          340          345          350
126 gaa gca cta aaa aaa gac ttt tct aac cct gat tat ggt gtc gat acg      1104
127 Glu Ala Leu Lys Lys Asp Phe Ser Asn Pro Asp Tyr Gly Val Asp Thr
128          355          360          365
130 cca tta gct cta aac aga tct caa tca aaa aat tca cca cat aag agt      1152

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132				370					375					380			
134	gca	agt	cca	cgc	atg	aat	tta	atg	agt	tta	gct	gct	gag	cct	aat	agt	1200
135	Ala	Ser	Pro	Arg	Met	Asn	Leu	Met	Ser	Leu	Ala	Ala	Glu	Pro	Asn	Ser	
136			385					390					395				
138	ggt	aaa	aat	gtg	aat	gat	aaa	ggt	aaa	atc	aca	aac	cct	acg	ctt	tca	1248
139	Gly	Lys	Asn	Val	Asn	Asp	Lys	Val	Lys	Ile	Thr	Asn	Pro	Thr	Leu	Ser	
140		400					405					410					
142	ctt	aat	aag	agt	aat	aat	cac	gct	aat	aac	gta	ata	tggt	cca	aca	agt	1296
143	Leu	Asn	Lys	Ser	Asn	Asn	His	Ala	Asn	Asn	Val	Ile	Trp	Pro	Thr	Ser	
144	415				420						425					430	
146	aac	gaa	caa	ttt	aat	tta	aaa	gca	aat	tat	gaa	tta	gat	gac	agc	ata	1344
147	Asn	Glu	Gln	Phe	Asn	Leu	Lys	Ala	Asn	Tyr	Glu	Leu	Asp	Asp	Ser	Ile	
148				435						440					445		
150	aaa	gag	gga	gat	act	ttt	act	att	aag	tat	ggt	cag	tat	att	aga	ccg	1392
151	Lys	Glu	Gly	Asp	Thr	Phe	Thr	Ile	Lys	Tyr	Gly	Gln	Tyr	Ile	Arg	Pro	
152			450						455				460				
154	ggt	ggt	tta	gaa	ctt	cct	gca	ata	aaa	act	caa	cta	cgt	agt	aag	gat	1440
155	Gly	Gly	Leu	Glu	Leu	Pro	Ala	Ile	Lys	Thr	Gln	Leu	Arg	Ser	Lys	Asp	
156		465					470					475					
158	ggc	tct	att	gta	gct	aat	ggt	gta	tat	gat	aaa	act	aca	aat	acg	acg	1488
159	Gly	Ser	Ile	Val	Ala	Asn	Gly	Val	Tyr	Asp	Lys	Thr	Thr	Asn	Thr	Thr	
160		480				485					490						
162	act	tat	aca	ttt	act	aac	tat	ggt	gat	caa	tat	caa	aat	att	aca	ggt	1536
163	Thr	Tyr	Thr	Phe	Thr	Asn	Tyr	Val	Asp	Gln	Tyr	Gln	Asn	Ile	Thr	Gly	
164	495				500					505						510	
166	agt	ttt	gat	tta	att	gcg	acg	cct	aag	agg	gaa	aca	gca	att	aag	gat	1584
167	Ser	Phe	Asp	Leu	Ile	Ala	Thr	Pro	Lys	Arg	Glu	Thr	Ala	Ile	Lys	Asp	
168				515					520						525		
170	aat	cag	aat	tat	cct	atg	gaa	gtg	acg	att	gct	aac	gaa	gta	gtc	aaa	1632
171	Asn	Gln	Asn	Tyr	Pro	Met	Glu	Val	Thr	Ile	Ala	Asn	Glu	Val	Val	Lys	
172			530						535				540				
174	aaa	gac	ttc	att	gtg	gat	tat	ggt	aat	aaa	aag	gac	aat	aca	act	aca	1680
175	Lys	Asp	Phe	Ile	Val	Asp	Tyr	Gly	Asn	Lys	Lys	Asp	Asn	Thr	Thr	Thr	
176		545					550					555					
178	gca	gcg	gta	gca	aat	gtg	gat	aat	gta	aat	aat	aaa	cat	aac	gaa	gtt	1728
179	Ala	Ala	Val	Ala	Asn	Val	Asp	Asn	Val	Asn	Asn	Lys	His	Asn	Glu	Val	
180		560				565						570					
182	ggt	tat	cta	aac	caa	aat	aac	caa	aac	cct	aaa	tat	gct	aaa	tat	ttc	1776
183	Val	Tyr	Leu	Asn	Gln	Asn	Asn	Gln	Asn	Pro	Lys	Tyr	Ala	Lys	Tyr	Phe	
184	575				580						585					590	
186	tca	aca	gta	aaa	aat	ggt	gaa	ttt	ata	cca	ggt	gaa	gtg	aaa	gtt	tac	1824
187	Ser	Thr	Val	Lys	Asn	Gly	Glu	Phe	Ile	Pro	Gly	Glu	Val	Lys	Val	Tyr	
188				595					600						605		
190	gaa	gtg	acg	gat	acc	aat	gcg	atg	gta	gat	agc	ttc	aat	cct	gat	tta	1872
191	Glu	Val	Thr	Asp	Thr	Asn	Ala	Met	Val	Asp	Ser	Phe	Asn	Pro	Asp	Leu	
192			610						615				620				
194	aat	agt	tct	aat	gta	aaa	gat	gtg	aca	agt	caa	ttt	gca	cct	aaa	gta	1920
195	Asn	Ser	Ser	Asn	Val	Lys	Asp	Val	Thr	Ser	Gln	Phe	Ala	Pro	Lys	Val	

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196	625	630	635	
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202	aat ggt aaa aag tat att gta act caa gca gtg aga cca acg gga act	2016		
203	Asn Gly Lys Lys Tyr Ile Val Thr Gln Ala Val Arg Pro Thr Gly Thr			
204	655 660 665 670			
206	gga aat gtt tat acc gaa tat tgg tta aca aga gat ggt act acc aat	2064		
207	Gly Asn Val Tyr Thr Glu Tyr Trp Leu Thr Arg Asp Gly Thr Thr Asn			
208	675 680 685			
210	aca aat gat ttt tac cgt gga acg aag tct aca acg gtg act tat ctc	2112		
211	Thr Asn Asp Phe Tyr Arg Gly Thr Lys Ser Thr Thr Val Thr Tyr Leu			
212	690 695 700			
214	aat ggt tct tca aca gca cag ggg gat aat cct aca tat agt cta ggt	2160		
215	Asn Gly Ser Ser Thr Ala Gln Gly Asp Asn Pro Thr Tyr Ser Leu Gly			
216	705 710 715			
218	gac tat gta tgg tta gat aaa aat aaa aac ggt gtt caa gat gat gat	2208		
219	Asp Tyr Val Trp Leu Asp Lys Asn Lys Asn Gly Val Gln Asp Asp Asp			
220	720 725 730			
222	gag aaa ggt tta gca ggt gtt tat gtt act ctt aaa gac agt aac aat	2256		
223	Glu Lys Gly Leu Ala Gly Val Tyr Val Thr Leu Lys Asp Ser Asn Asn			
224	735 740 745 750			
226	aga gaa tta caa cgt gta act act gat caa tct gga cat tat caa ttt	2304		
227	Arg Glu Leu Gln Arg Val Thr Thr Asp Gln Ser Gly His Tyr Gln Phe			
228	755 760 765			
230	gat aat tta caa aat gga acg tac aca gtc gag ttt gcg att cct gat	2352		
231	Asp Asn Leu Gln Asn Gly Thr Tyr Thr Val Glu Phe Ala Ile Pro Asp			
232	770 775 780			
234	aat tat acg cca tct ccc gca aat aat tct aca aat gat gca ata gat	2400		
235	Asn Tyr Thr Pro Ser Pro Ala Asn Asn Ser Thr Asn Asp Ala Ile Asp			
236	785 790 795			
238	tca gat ggt gaa cgt gat ggt aca cgt aaa gta gtt gtt gcc aaa gga	2448		
239	Ser Asp Gly Glu Arg Asp Gly Thr Arg Lys Val Val Val Ala Lys Gly			
240	800 805 810			
242	aca att aat aat gct gat aat atg act gta gat act ggc ttt tat tta	2496		
243	Thr Ile Asn Asn Ala Asp Asn Met Thr Val Asp Thr Gly Phe Tyr Leu			
244	815 820 825 830			
246	act cct aaa tac aat gtc gga gat tat gta tgg gaa gat aca aat aaa	2544		
247	Thr Pro Lys Tyr Asn Val Gly Asp Tyr Val Trp Glu Asp Thr Asn Lys			
248	835 840 845			
250	gat ggt atc caa gat gac aat gaa aaa gga att tct ggt gtt aaa gta	2592		
251	Asp Gly Ile Gln Asp Asp Asn Glu Lys Gly Ile Ser Gly Val Lys Val			
252	850 855 860			
254	acg tta aaa aat aaa aat gga gat act att ggc aca acg aca aca gat	2640		
255	Thr Leu Lys Asn Lys Asn Gly Asp Thr Ile Gly Thr Thr Thr Asp			
256	865 870 875			
258	tca aat ggt aaa tat gaa ttc aca ggt tta gag aac ggg gat tac aca	2688		
259	Ser Asn Gly Lys Tyr Glu Phe Thr Gly Leu Glu Asn Gly Asp Tyr Thr			
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263	Ile	Glu	Phe	Glu	Thr	Pro	Glu	Gly	Tyr	Thr	Pro	Thr	Lys	Gln	Asn	Ser	
264	895					900					905					910	
266	gga	agt	gac	gaa	ggg	aaa	gat	tca	aac	ggg	acg	aaa	aca	aca	gtc	aca	2784
267	Gly	Ser	Asp	Glu	Gly	Lys	Asp	Ser	Asn	Gly	Thr	Lys	Thr	Thr	Val	Thr	
268					915					920						925	
270	gtc	aaa	gat	gca	gat	aat	aaa	aca	ata	gac	tca	ggg	ttc	tac	aag	cca	2832
271	Val	Lys	Asp	Ala	Asp	Asn	Lys	Thr	Ile	Asp	Ser	Gly	Phe	Tyr	Lys	Pro	
272				930					935					940			
274	aca	tat	aac	tta	ggg	gac	tat	gta	tgg	gaa	gat	aca	aat	aaa	gat	ggg	2880
275	Thr	Tyr	Asn	Leu	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn	Lys	Asp	Gly	
276			945					950					955				
278	att	caa	gac	gac	agt	gaa	aaa	ggg	att	tct	ggg	gtt	aaa	gtg	acg	tta	2928
279	Ile	Gln	Asp	Asp	Ser	Glu	Lys	Gly	Ile	Ser	Gly	Val	Lys	Val	Thr	Leu	
280		960					965					970					
282	aaa	gat	aaa	aat	gga	aat	gcc	att	ggg	aca	acg	aca	aca	gac	gca	agt	2976
283	Lys	Asp	Lys	Asn	Gly	Asn	Ala	Ile	Gly	Thr	Thr	Thr	Thr	Asp	Ala	Ser	
284	975				980					985					990		
286	ggg	cat	tat	caa	ttt	aaa	gga	tta	gaa	aat	gga	agc	tac	aca	gtt	gag	3024
287	Gly	His	Tyr	Gln	Phe	Lys	Gly	Leu	Glu	Asn	Gly	Ser	Tyr	Thr	Val	Glu	
288				995					1000						1005		
290	ttt	gag	aca	cca	tca	ggg	tat	aca	ccg	aca	aaa	gcg	aat	tca	ggg		3069
291	Phe	Glu	Thr	Pro	Ser	Gly	Tyr	Thr	Pro	Thr	Lys	Ala	Asn	Ser	Gly		
292				1010					1015					1020			
294	caa	gat	ata	act	gta	gat	tcc	aac	ggg	ata	aca	aca	aca	ggg	atc		3114
295	Gln	Asp	Ile	Thr	Val	Asp	Ser	Asn	Gly	Ile	Thr	Thr	Thr	Gly	Ile		
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298	att	aac	gga	gct	gat	aat	ctc	aca	att	gat	agt	ggg	ttc	tac	aaa		3159
299	Ile	Asn	Gly	Ala	Asp	Asn	Leu	Thr	Ile	Asp	Ser	Gly	Phe	Tyr	Lys		
300				1040					1045					1050			
302	aca	cca	aaa	tat	agt	gtc	gga	gat	tat	gta	tgg	gaa	gat	aca	aat		3204
303	Thr	Pro	Lys	Tyr	Ser	Val	Gly	Asp	Tyr	Val	Trp	Glu	Asp	Thr	Asn		
304				1055					1060					1065			
306	aaa	gat	ggg	atc	caa	gat	gac	aat	gaa	aag	gga	att	tct	ggg	gtt		3249
307	Lys	Asp	Gly	Ile	Gln	Asp	Asp	Asn	Glu	Lys	Gly	Ile	Ser	Gly	Val		
308				1070					1075					1080			
310	aaa	gta	acg	tta	aag	gat	gaa	aaa	gga	aat	ata	att	agc	act	aca		3294
311	Lys	Val	Thr	Leu	Lys	Asp	Glu	Lys	Gly	Asn	Ile	Ile	Ser	Thr	Thr		
312				1085					1090					1095			
314	aca	act	gat	gaa	aat	ggg	aag	tat	caa	ttt	gat	aat	tta	gat	agt		3339
315	Thr	Thr	Asp	Glu	Asn	Gly	Lys	Tyr	Gln	Phe	Asp	Asn	Leu	Asp	Ser		
316				1100					1105					1110			
318	ggg	aat	tac	att	att	cat	ttt	gag	aaa	ccg	gaa	ggc	atg	act	caa		3384
319	Gly	Asn	Tyr	Ile	Ile	His	Phe	Glu	Lys	Pro	Glu	Gly	Met	Thr	Gln		
320				1115					1120					1125			
322	act	aca	gca	aat	tct	gga	aat	gat	gat	gaa	aaa	gat	gct	gat	ggg		3429
323	Thr	Thr	Ala	Asn	Ser	Gly	Asn	Asp	Asp	Glu	Lys	Asp	Ala	Asp	Gly		
324				1130					1135					1140			
326	gaa	gat	gtt	cgt	gtt	acg	att	act	gat	cat	gat	gac	ttt	agt	ata		3474

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:15; N Pos. 6,12

Seq#:17; Xaa Pos. 3

**VERIFICATION SUMMARY**

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Input Set : A:\Sequence\_10-615,383.txt

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L:37 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:35  
L:903 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:901  
L:1452 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:13,Line#:1450  
L:1725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
L:1751 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0